

Supplemental Material to:

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**Functional consequences of microbial shifts in the human
gastrointestinal tract linked to antibiotic treatment and
obesity**

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Supplementary Files

- 2 Supplementary File includes:
 Supplementary Figures S1 to S3
- 4 Supplementary Tables S1 to S5

Supplementary Figures

Figure S1. Relative contribution of the abundance level of glycoside-hydrolase like enzyme recovered from each of the shotgun metaproteomes of one patient (P1) receiving β -lactam therapy. The abundance values of GH-like enzymes (183 in total), from a total number of 3,011 proteins that were unambiguously quantified in the same set of samples used for activity tests, were considered: FS-0, 211; FS-3, 186; FS-6, 188; FS-11, 158; and FS-14, 199. Abbreviations as follows: GHx, family of Glycoside-Hydrolases; CBM, Carbohydrate-Binding Module. Results are the average of two independent technical replicates per sample and graphs was plotted using mean values with the standard deviation lower than 2%. Note: Predicted GH-like enzymes and CBMs were identified (and manually analyzed) in the shotgun metaproteomes via the Basic Local Alignment Search Tool Protein (BLASTP) analysis against the Carbohydrate Active Enzyme database,²³ according to an E-value $<e^{-05}$ and a sequence homology $\geq 50\%$.

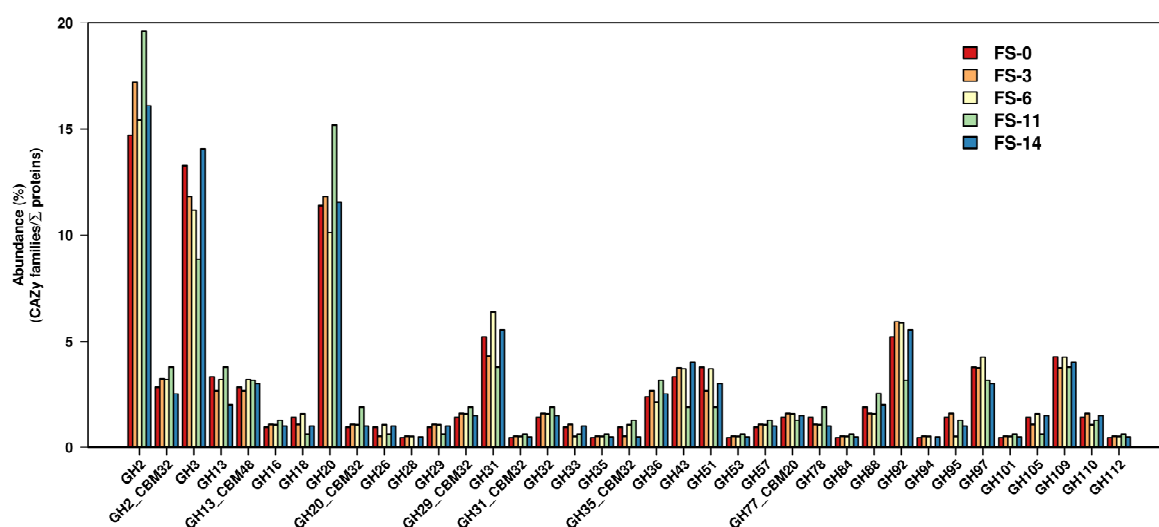


Figure S2. Antibiotic-mediated community behavior characterized by mapping to metabolic pathways. Proteome-scale metabolic reconstructions were based on the expression values of a set of proteins with Enzyme Commission (EC) number that were found among the 3,011 proteins that were unambiguously quantified in the metaproteomes of all the P1 samples (receiving β -lactam therapy).¹⁰ Ad-hoc computer programs written in C and Perl were used to obtain information from local copies of KEGG and to generate the graphical representations. The following color code was used: green, increased expression; red, decreased expression and thickness was proportional to the ratio. Maps were generated based on the expression level of proteins found in samples FS-3 (A), FS-6 (B), FS-11 (C) and FS-14 (D) compared to the values in FS-0. This Figure is provided as separate file (scalable PDF version) to ensure high quality resolution.

Figure S3. Obesity-mediated community behavior characterized by mapping to metabolic pathways. Proteome-scale metabolic reconstructions were based on the expression values of a set of proteins with Enzyme Commission (EC) number that were found among the 613 proteins that were unambiguously quantified in the metaproteomes of one obese adolescent (Obese111) and one lean adolescent (LeanCE01).⁶ Ad-hoc computer programs written in C and Perl were used to obtain information from local copies of KEGG and to generate the graphical representations. The following color code was used: green, increased expression; red, decreased expression and thickness was proportional to the ratio. Maps were generated based on the expression level of proteins found in obese compared to the values in lean. This Figure is provided as separate file (scalable PDF version) to ensure high quality resolution.

Supplementary Tables

Table S1 Biochemical measures and general characteristics of antibiotic-treated patients as well as obese and lean individuals investigated in the present study.

Sample ¹	Age	Sex ²	Weight (kg)	Height (cm)	BMI (kg/m ²)	Fasting glucose (mg/dL)	Fasting insulin (pg/mL)	HOMA-IR ³	Uric acid (mg/dL)	Total cholesterol (mg/dL)	HDL cholesterol (mg/dL)	LDL cholesterol (mg/dL)	Tryglicerides (mg/dL)
Obese110	13	M	66.2	161.6	25.35	82	14.9	0.07	5.4	118	51	47	100
Obese111	15	M	102.7	171	35.12	80	17.5	0.09	8.6	198	46	118	172
Obese116	16	F	85.95	165.8	31.27	83	13.7	0.07	5.3	131	49	70	59
Obese122	14	M	108.2	181.5	32.85	86	30.9	0.16	8.1	139	50	77	59
Obese125	16	F	74.2	173	24.79	83	9.2	0.05	4.5	147	66	68	67
Obese128	14	F	71.6	165.5	26.14	79	12	0.06	6.3	119	43	66	48
Obese129	15	M	100.2	174	33.1	84	23.1	0.12	6.5	197	45	120	160
LeanCE01	15	F	63.1	165	23.18	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LeanCE03	13	M	40.9	151	17.94	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LeanCE05	16	F	61.5	162	23.43	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LeanCE07	16	F	58.1	157	23.57	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
LeanCE09	15	M	65.9	173	22.02	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
P1	68	M	105	177	33.5	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
P2	73	F	54.0	156	22.20	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

¹Note: Biochemical measures and general characteristics of individuals P1, P2, Obese111 and leanCE01 have been previously described; for details see ref. 6 and 10 (main text).

²Abbreviations as follows: M, male; F, female

³HOMA-IR index was calculated using a free web HOMA-IR calculator available at <http://www.hcvsociety.org/files/HOMACalc.htm>
n.a. Data not available.

Table S2 Differences in the relative contribution of carbohydrate turnovers. Combine shifts during the antibiotic treatment as compared to the admission day and shifts between obese and lean subjects are specifically indicated. The relative activity level was calculated per each sample according to the data provided in Fig. 1 and mean values from three independent measurements per group of samples are given.

Sugar substrate	Relative contribution (%) of glycosidase activities referred to the total ¹						
	FS-0 (n=2)	FS-3 (n=2)	FS-6 (n=2)	FS-11 (n=2)	FS-14 (n=2)	Obese (n=7)	Lean (n=5)
α -Glucose	4.96	2.11	2.90	0.42	3.06	7.76	1.40
β -D-Glucose	3.61	1.63	3.78	6.14	5.73	7.33	4.94
α -Maltose	2.89	1.10	1.53	2.08	1.83	4.63	7.85
α -D-Maltopentose	2.60	1.21	1.20	0.87	1.15	2.87	4.71
α -D-Maltohexose	5.89	1.72	2.24	4.47	2.75	2.87	4.47
β -D-Cellobiose	0.19	0.17	0.24	0.13	0.19	2.05	4.27
α -L-Galactose	13.64	26.12	15.60	16.54	17.59	19.72	18.48
β -D-Galactose	39.52	55.60	49.54	31.08	47.57	19.50	13.70
α -Xylose	1.06	0.22	0.26	0.13	0.23	0.55	0.64
β -Xylose	0.34	0.28	2.21	0.17	0.39	5.69	9.47
α -Arabinopyranose	4.27	2.54	4.23	4.77	5.48	1.26	4.03
β -Arabinopyranose	0.34	0.16	0.15	0.11	0.19	0.48	0.43
α -Arabinofuranose	2.84	2.09	3.52	1.61	2.19	11.03	1.07
α -L-Rhamnose	0.88	0.62	2.32	1.89	0.67	1.59	4.24
α -Mannose	11.91	1.49	3.10	11.33	4.37	2.86	2.86
β -D-Mannose	0.77	0.12	0.41	0.42	0.54	0.53	0.93
β -Lactose	1.25	1.21	1.46	1.95	2.62	6.43	8.22
α -Fucose	0.24	0.19	0.64	0.21	0.17	1.15	1.94
β -Fucose	2.10	1.88	2.36	3.41	3.13	1.11	5.26
β -Glucuronide	0.08	0.02	0.13	0.08	0.07	0.34	0.24
β -Acetylglucuronide	0.11	0.05	0.13	0.06	0.06	0.23	0.30
α -Acetylneuraminic acid	0.24	0.04	1.23	5.58	0.01	0.01	0.26
β -N-Acetyl- β -D-glucosaminide	0.28	0.05	0.80	6.55	0.02	0.02	0.32

¹Standard deviation (SD) ranging (refer to the relative contribution [%]) from 0.33 to 1.69x10⁻⁵ (for FS-0; n=2, three replicates each), 0.21 to 7.7x10⁻⁵ (for FS-3; n=2, three replicates each), 0.30 to 1.3x10⁻⁴ (for FS-6; n=2, three replicates each), 0.25 to 2.9x10⁻⁵ (for FS-11; n=2, three replicates each), 0.43 to 1.8x10⁻⁵ (for FS-14; n=2, three replicates each), 1.0 to 8.0x10⁻⁴ (for obese; n=5, three replicates each) and 1.0 to 0.0023 (for lean; n=7, three replicates each).

Table S3. Proteomic-based responses to KEGG reactions during the 14-days β -lactam therapy of P1. A detailed analysis of the KEGG reactions found to be differentially activated or deactivated and appearing or disappearing as compared to the sample before the beginning of the therapy (day 0), on relative concentration of protein basis, is specifically shown. Fold changes (FC), calculated as the average of protein expression levels of proteins assigned to the same reaction in samples FS-3, FS-6, FS-11 and FS-14 as compared to FS-0, are also provided. Note: the terms “activated” and “deactivated” refer to the number of metabolic reactions that were up- or down-regulated, respectively, by considering a threshold of at least 1.5 fold change in abundance levels of the corresponding pooled proteins belonging to a particular reaction, as compared with the initial sample (day 0); the term “new” refers to the number of reactions containing proteins that were only expressed in samples FS-3 to FS-14 as compared to FS-0; the term “disappear” refers to the number of reactions containing proteins that were only expressed in samples FS-0 as compared to FS-3 to FS-14.

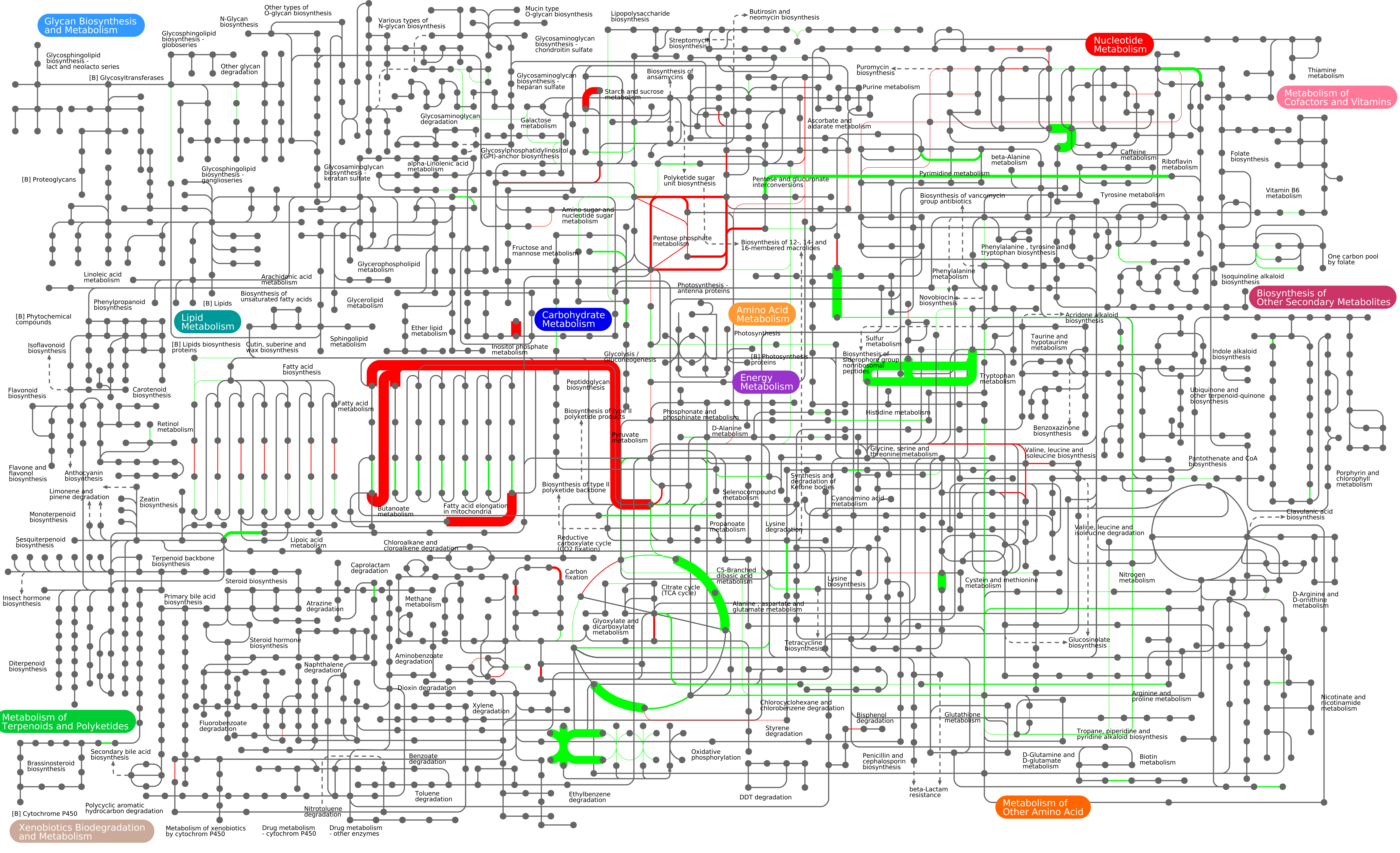
t (days)	Number of reactions		Number of activated/deactivated reactions according to fold changes (FC) groups				
	Activated	New	$1.5 < FC < 5$	$5 \leq FC < 10$	$10 \leq FC < 15$	$15 \leq FC < 20$	$20 \leq FC$
FS-3	116	12	65	19	6	1	13
FS-6	90	11	39	20	4	3	13
FS-11	47	7	29	3	3	1	4
FS-14	93	11	57	12	4	0	9
	Deactivated	Disappear	$1.5 < 1/FC < 5$	$5 \leq 1/FC < 10$	$10 \leq 1/FC < 15$	$15 \leq 1/FC < 20$	$20 \leq 1/FC$
FS-3	50	8	26	7	2	1	6
FS-6	63	1	43	8	2	5	4
FS-11	121	20	40	18	7	7	29
FS-14	61	3	38	11	5	2	2

Table S4. Proteomic-based responses to KEGG pathways during the 14-days β -lactam therapy of P1. The changes in the number of pathways were computed as a function of the number of up- and down-regulated reactions in each pathway, by considering a threshold of at least 1.5 fold changes in abundance levels of the corresponding pooled proteins. The table presents the differences between the number of up- and down-regulated reactions, therefore a positive number is interpreted as a signal of pathway upregulation, whereas a negative number indicates and overall pathway down-regulation. For additional quantification of selected pathways see Table S5.

KEGG pathway	Kegg ID	FS-3	FS-6	FS-11	FS-14
Glycolysis / Gluconeogenesis	ec00010	0	-1	-9	0
Citrate cycle (TCA cycle)	ec00020	2	1	-3	2
Pentose phosphate pathway	ec00030	3	2	-5	3
Fructose and mannose metabolism	ec00051	-1	1	-7	5
Fatty acid metabolism	ec00071	-1	-1	-3	-2
Alanine, aspartate and glutamate metabolism	ec00250	9	6	-12	1
Glycine, serine and threonine metabolism	ec00260	3	-1	-6	2
Cysteine and methionine metabolism	ec00270	3	1	-3	0
Valine, leucine and isoleucine degradation	ec00280	-2	-2	-4	-2
Arginine and proline metabolism	ec00330	8	5	-3	3
Phenylalanine, tyrosine and tryptophan biosynthesis	ec00400	3	3	-2	0
Cyanoamino acid metabolism	ec00460	1	1	-4	1
Starch and sucrose metabolism	ec00500	3	2	-2	1
Other glycan degradation	ec00511	5	1	1	1
Various types of N-glycan biosynthesis	ec00513	1	1	1	0
Amino sugar and nucleotide sugar metabolism	ec00520	7	7	-2	4
Glyoxylate and dicarboxylate metabolism	ec00630	0	-3	-7	-3
One carbon pool by folate	ec00670	1	-1	-2	-2
Carbon fixation pathways in prokaryotes	ec00720	0	1	-6	1
Vitamin B6 metabolism	ec00750	1	1	1	1
Isoquinoline alkaloid biosynthesis	ec00950	1	1	0	-1
Tropane, piperidine and pyridine alkaloid biosynthesis	ec00960	1	1	0	-1
Drug metabolism - other enzymes	ec00983	2	0	-1	0
Oxidative phosphorylation	ec00190	1	3	0	2
Histidine metabolism	ec00340	1	-1	-1	0
D-Alanine metabolism	ec00473	1	1	-1	1
Lipopolysaccharide biosynthesis	ec00540	0	0	-2	1
Glycerolipid metabolism	ec00561	0	1	-2	-1
Biotin metabolism	ec00780	1	1	-1	1
Retinol metabolism	ec00830	1	1	-1	0
Galactose metabolism	ec00052	1	0	2	-1
Tyrosine metabolism	ec00350	2	2	-1	-1
Glycosaminoglycan degradation	ec00531	2	0	2	-1
Sphingolipid metabolism	ec00600	1	-2	-1	-2
Riboflavin metabolism	ec00740	2	2	-2	2
Lysine biosynthesis	ec00300	2	0	-2	2
Glutathione metabolism	ec00480	3	4	-2	2
Purine metabolism	ec00230	-2	-4	-7	-4
Pyrimidine metabolism	ec00240	1	2	-6	-2
Nitrogen metabolism	ec00910	6	6	-9	3
Inositol phosphate metabolism	ec00562	-1	0	-2	0
Taurine and hypotaurine metabolism	ec00430	-1	-2	-4	-1
Valine, leucine and isoleucine biosynthesis	ec00290	-1	-2	-2	-1

Table S5. Relative changes in selected pathways referred to FS-0. The changes in each pathway have been estimated by pooling the changes in all the enzymes (characterized by their EC codes) assigned to the corresponding pathway. Data refer to samples from patient P1.

Kegg ID	KEGG metabolism/pathway	Fold change in expression of proteins assigned to KEGG metabolism/pathway			
		FS-3 vs FS0	FS-6 vs FS0	FS-11 vs FS0	FS-14 vs FS0
	Carbohydrate metabolism				
ec00010	Glycolysis / Gluconeogenesis	3.701	5.411	-32.232	3.290
ec00020	Citrate cycle (TCA cycle)	54.715	42.290	-4.508	52.389
ec00030	Pentose phosphate pathway	3.693	7.828	-17.839	7.778
ec00040	Pentose and glucuronate interconversions	0.433	1.121	-9.139	1.958
	Energy metabolism				
ec00190	Oxidative phosphorylation	22.676	24.426	-3.278	23.486
	Nucleotide metabolism				
ec00230	Purine metabolism	30.566	22.206	-40.882	23.132
ec00240	Pyrimidine metabolism	29.593	30.369	-65.126	18.793
	Amino acid metabolism				
ec00250	Alanine, aspartate and glutamate metabolism	22.223	16.990	-117.436	5.145
ec00260	Glycine, serine and threonine metabolism	0.275	-3.544	-26.805	-3.516
ec00270	Cysteine and methionine metabolism	26.133	2.501	-0.559	-5.523
ec00290	Valine, leucine and isoleucine biosynthesis	-0.416	-4.307	-13.557	1.961
ec00300	Lysine biosynthesis	22.215	18.723	0.822	19.770
ec00330	Arginine and proline metabolism	23.467	18.151	-2.652	13.455
ec00340	Histidine metabolism	3.876	-0.913	-24.986	1.723
ec00350	Tyrosine metabolism	5.644	6.940	-1.580	-2.206
ec00360	Phenylalanine metabolism	3.458	4.273	1.020	-1.858
ec00380	Tryptophan metabolism	-16.417	-18.035	-18.360	8.528
ec00400	Phenylalanine, tyrosine and tryptophan biosynthesis	8.478	7.169	-3.403	-0.463



Glycan Biosynthesis and Metabolism

N-Glycan biosynthesis
Other types of O-glycan biosynthesis
Various types of N-glycan biosynthesis
Mucin type O-glycan biosynthesis
Lipopolysaccharide biosynthesis
Butirosin and neomycin biosynthesis
Streptomycin biosynthesis
Biosynthesis of ansamycins
Purine metabolism
Purine biosynthesis
Ascorbate and aldarate metabolism
Pyrimidine metabolism
beta-Alanine metabolism
Caffeine metabolism
Riboflavin metabolism
Folate biosynthesis
Vitamin B6 metabolism
One carbon pool by folate
Isoquinoline alkaloid biosynthesis
Indole alkaloid biosynthesis
Ubiquinone and other terpenoid-quinone biosynthesis
Pantothenate and CoA biosynthesis
Porphyrin and chlorophyll metabolism
Clavulanic acid biosynthesis
Valine, leucine and isoleucine degradation
Nitrogen metabolism
Arginine and proline metabolism
Biotin metabolism
D-Glutamine and D-glutamate metabolism
Tropine, piperidine and pyridine alkaloid biosynthesis
Glutathione metabolism
Penicillin and cephalosporin biosynthesis
beta-Lactam resistance
DDT degradation
Oxidative phosphorylation
Styrene degradation
Chlorocyclohexane and chlorobenzene degradation
Bisphenol degradation
Toluene degradation
Ethylbenzene degradation
Nitrotoluene degradation
Polycyclic aromatic hydrocarbon degradation
Secondary bile acid biosynthesis
Brassinosteroid biosynthesis
[B] Cytochrome P450

Lipid Metabolism

Carbohydrate Metabolism

Amino Acid Metabolism

Energy Metabolism

Nucleotide Metabolism

Metabolism of Cofactors and Vitamins

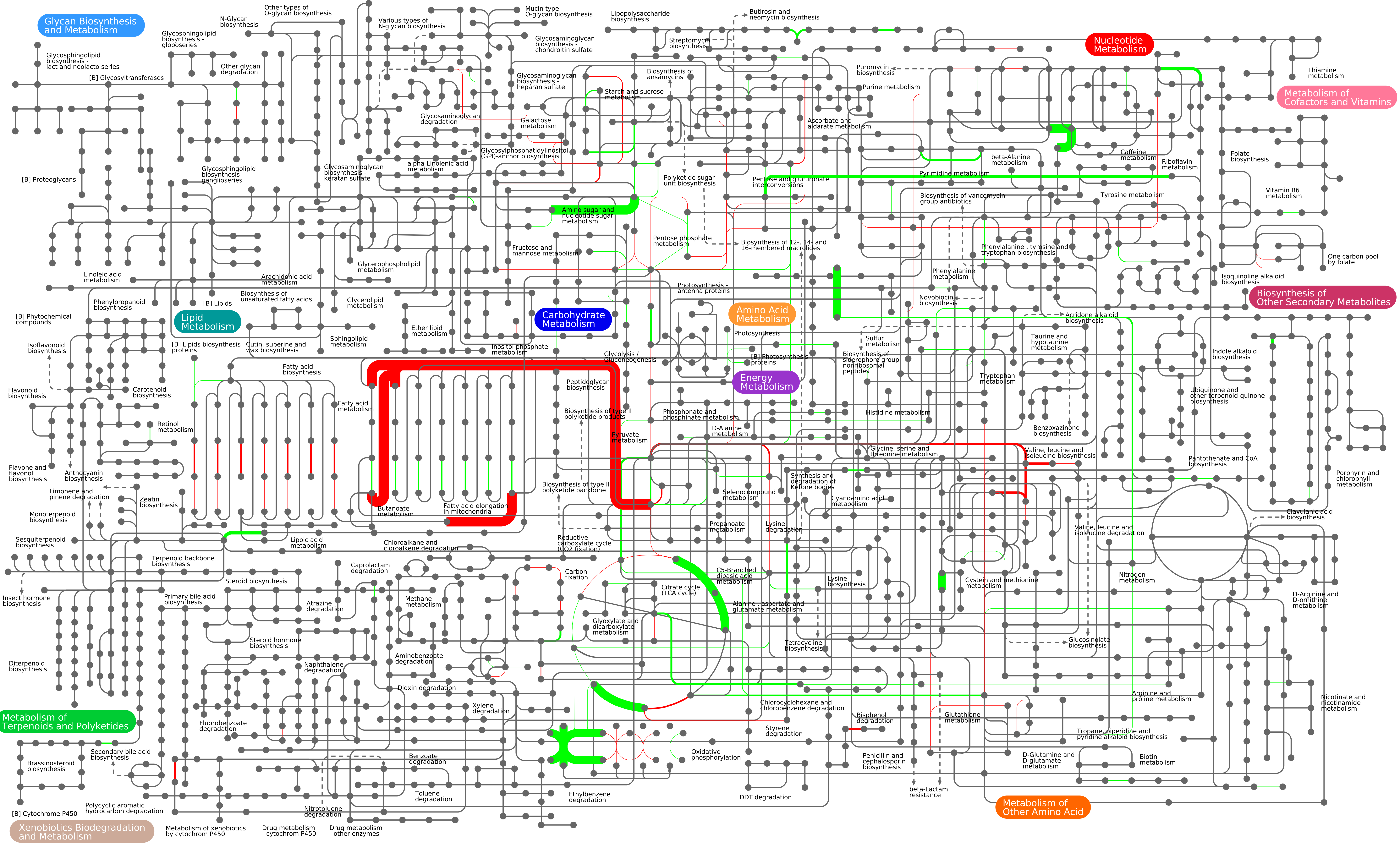
Biosynthesis of Other Secondary Metabolites

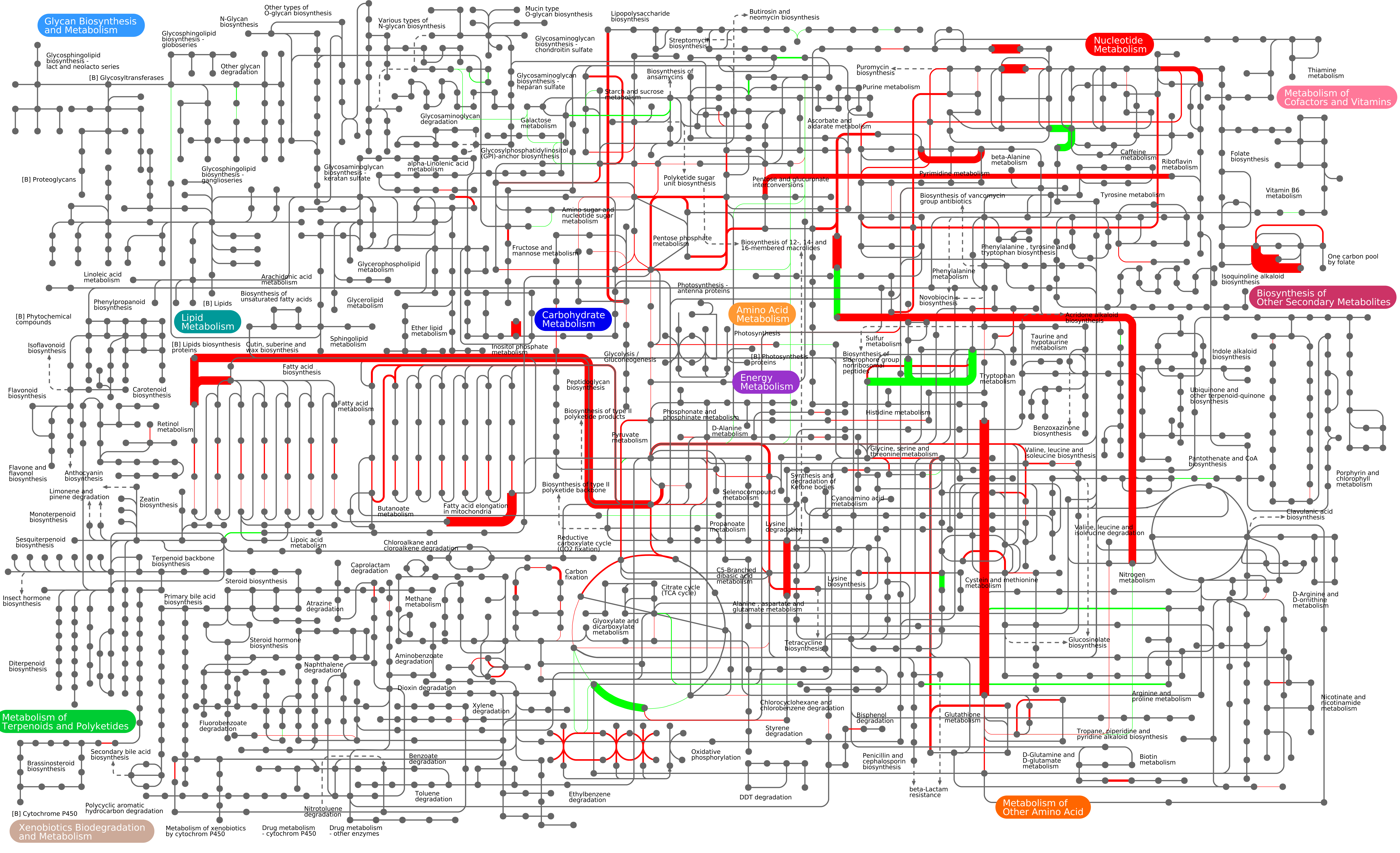
Metabolism of Terpenoids and Polyketides

Xenobiotics Biodegradation and Metabolism

Metabolism of Other Amino Acid

Metabolism of xenobiotics by cytochrome P450
Drug metabolism - cytochrome P450
Drug metabolism - other enzymes





Glycan Biosynthesis and Metabolism

Lipid Metabolism

Carbohydrate Metabolism

Amino Acid Metabolism

Energy Metabolism

Nucleotide Metabolism

Metabolism of Cofactors and Vitamins

Biosynthesis of Other Secondary Metabolites

Metabolism of Terpenoids and Polyketides

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